

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCCCGCGCCGGAGGCCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT
GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAAGTGTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCGCCGCGAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
GCCCTCCCGGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCC
CGTGGAATATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGTTGTTCTTA
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLLPPAPEAAKKPTPCRRCGLVDKFNQGMVDTAKKNFGGGNTAWEEKTL SKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFVCVKTLKVCCSPGTYPGDCCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGVWLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA EKT
CVRKNENCYNTPGSYVCVCPDGFEE TEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCTGAGCAGC**ATGG**CCCCGAGGAGCGCCTTC
CCTGCCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCCTGTCCTTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTTTCCCATGTCTTGAAAAACAGGATGGGGTGGCAGCATTTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCCAAACACCTCAAAATGCTATCT
TCTTTAAAACATGTCAACAAGCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACGTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACC
TGTTTTCTACCCTGGAAAAATGATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCCACAAACCCTGTGCAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT
GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATAATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTAAACCTTTCA
TGTGTTGAATGTTCAAATAATGTTTCATTACACTTAAGAATACTGTCCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTTTCTTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAATTACAATGCATTTATGGT
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAGATTTTATTGTCAGATATTTAGAT
GTTTGTTACATTTTTTAAAAATTGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACC
TTACCATTATTCCAGAGATTCAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTTGTCAT
TGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094

><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEEERDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTG

CGGACGCGTG GGGCGTCCGGCGGTTCG CAGAGCCAGGAGGCGGAGGCGCGGGGCCAGCCTGGG
CCCCAGCCCACACCTTCACCAGGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCTGTATCTA
TCCAGTCTTGGAACGTACTGGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTTCTGGGGCATGACCCTGGATTGAGGGCATTCGCTACCGCCTGGGCACCA
TCCGCCCATCTTCCCTCGGTGATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG
GTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCTGTCTGTGCGCCCAAGACCTGCTGTCTTGTGAC
ACCCACCAGCAGAGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTGC
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGAATGCGGCCAACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGAG
AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCTACTGAGGCTG
CGGGCACACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
GGGCGGTGACCCACGCTCGCCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG
GAGCCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTC
AGTGACCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC
TAATTTTTTGATTTTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCCAGGCTGGTTTCGAACT
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA
TAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCCTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACCTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCAGTGGGAGCCTGTCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCCTCCAACCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

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FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPSSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFFAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

[illegible]

CCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGAAGCA
CGTGCAGGTCACCGGGCGTTCGATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAG
TCATAGTGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTACGAGATCGTGCTGGAGAACTATACGGCCTTCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACCCGCCGACCAAGCGCACAC
GGCGGGCCCCAGCCCCCTACGTTAGTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCCGCCTCCC
CACCCCTTTCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGGCCGCGAAGCATCCGAGCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTGAGCGACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTTGTGTTTGTGTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAAATAG
AGGGTTGTCCACTCCTCACATTCACGACCCAGGCCTGCACCCCAACCCCAACTCCCAGCCC
CGGAATAAAACCATTTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLENNYTAFQONARHEGWFMATFRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGATTTTGTCTGTTTATTTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT
TTCCGTACTTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCCCT
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC
TGGATTTCCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC
AATATTAGACCATTTTACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
CACCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT
AAACCACATTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCCTGAACAAGTCCGGG
GGATGGCCGTGAGGGAATTAAATATGAATCTTTTGTCTGTCCACCACGACCCCCGGCCTG
CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT
TCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTCTACCACATCGAAACTTCCCACGATTC
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCCACGTGATGGCATA
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTCCAGAGGC
CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
CCAGAAGTGGAAATACAACCGGGGCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGAT
CAACTCCTTAAAGGAGATTTTCACTGTCAGCCCATTTTACACCCCAAATGGGGGCATTAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTGCATATAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTGTAACTCTTTGCTTTTTTAAATCTT

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCOGPEQVRGMVRELMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGREVRTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCCTCGCCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC
TCGCTTCCCAGGCGCCGCGGCTGCAGCCTTGCCCCCTTTGCTCGCCTTGAAAAATGGAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTACGTGGGAGGTCCATCT
CTAGGGGCGACACGCTCGGACCCACCCGACAGCGGCCCTTCTGGAGAGTTCTGTGAGAACAAAGCGGGCAGACC
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTTCATCGTGGACA
TCTTGCAATTCTTGACATTGGTCCTGATGTCAACCGAGTGGGCCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCCGGCCCCCTGA
GGGAGAATGTGCCACGGGTCATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAATTTACGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT
GTGCCATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGTACAGTG
TCATACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAAACACGGATGTGAAC
ATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAAA
CGTGACACAAGGATCAACTACTGTGCACTGAACAAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCGTCTGCCAGTGTCTAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCCGGTGGATTACTGCCCTGTGAGTGACCATGGTTGTGAATACTCCT
GTGTCAACATGGACAGATCCTTTGCCTGTGAGTGTCTGAGGGACACGTGCTCCGACGCGATGGGAAGACGTGTG
CAAAATTGGACTCTTGTGCTCTGGGGGACACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTCTGTTTGTGT
GCCAGTGCTTTGAAGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCCAACACATTTGTGTTA
ATAATGGGAATTCTTACATCTGCAAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACCGGTGCAAGAAAT
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCTG
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGTCTCCAGT
ATTCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTTACCCAAG
GAGAAGGGGCCAGGCCCTTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCCGACGGACGGGCTCAGGATG
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAACACAAAGAGATTGCCTCTGAGCCCAACAAACAGCATCTCTTCTATGCCGAAGACTTCAGCACAAATGG
ATGAGATAAGTGAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAAC TGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTTTGCACTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT
GAACGCACTGCAGAGCCCCAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAACAATCAGTACTGA
GAAACCTGGTTTGCCACAGAACAAAGACAAGAAGTATACACTAATCTGTATAAATTTATCTAGGAAAAAATCCT
TCAGAATTTCAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC
AACTTGCTTCTGCCTCATCCTTACCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGCAAGTCTTACTT
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG
CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAAATTCACCACTTCAG

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Signal peptide:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Amidation site.

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCAGTGCCTCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGP RP GALTP T PSLSSQALPSPRLPTTDGAHPQPI SPIPGGVSSSGLSR
MGAVPVMVPAQSQAAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

[illegible][illegible]

FIGURE 19

MKRLPLL VVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLOEVYRNSVTDLSPTDIITYIEILAESSSLLGYKNNTISAKDTL
SNSTLT EFKTVNNFVQRDTFVVWDKLSVNHRRLTKLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFLYYK SIGPLLS
SSDNFLLKPQNYDNSEEEERVISVISVSMSSNPPTLYELEKITFTLSHRKVTD RYRSLCAF
WNYSPTMNGSWSSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL
LHYFFLAFAWMCIEGIHLYLIVGV IYNKGFLHKNFYIFGYLSPAVVVGFS AALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACCTTC
TGTTCTTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLEIKAVALLRTVAIKGVHVSRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

Abstract

Abstract

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
NSSYTMNTKTGTTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWAAAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

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GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
 AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCTTGGCAT
 CATGCTGCTATTTCCTGCAAATACTGAAGAAGCATGGGATTTAAATATTTTTACTTCTAAATAA
 ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
 TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTTTGGACAATG
 CAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAAAC'TTTGTGGTTCTATGGCATTTCATCA
 TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
 TGGAAATCCTTAAGGGCCCATTAACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
 CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
 TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT
 ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC
 AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG
 ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAAACAATTTATCTTCAGTCACCAAT
 ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGA
 ACTGCCTGAAAAATGTCTGTCCGAACCTGAGCAACTTACAAGAACTCTATATTAATCACAAC
 TGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC
 AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT
 TCTGATGATTGGGGAAAAATCCAATTATCAGAATCAAAGACATGAAC'TTTAAGCCTCTTATCA
 ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT
 GGACTGGAAAACCTTAGAAAGCATCTCTTTTTTACGATAACAGGC'TTATTAAGTACCCCATGT
 TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTTGGATCTAAATAAAAAATCCTATTAATAGAA
 TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAAATAATATGCCT
 GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
 TACTAACAAACCCTAGATTGTCTTACATTCACCCCAATGCATTTTTTTCAGACTCCCCAAGCTGG
 AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
 CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTG
 GATGAACATGAACAAAACCAACATTCGATTTCATGGAGCCAGATTCAGTGT'TTTGCGTGGACC
 CACCTGAATTCCAAGGTCAGAATGTTTCGGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT
 CTCCCTCTTATAGCTCCTGAGAGCTTTTCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
 TTCTTTTCACTGTAGAGCTACTGCAGAACCAAGCCTGAAATCTACTGGATAAACCTTCTG
 GTCAAAAACCTCTTGCCTAATACCTTGACAGACAAGTTCTATGTCCATTCTGAGGGAACTACTA
 GATATAAATGGCGTAACCTCCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT
 TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
 GCTCTTTGAATATTAATAAAGAGATATTTCAGGCCAATTCAGTTTTTGGTGTCTTGGAAAGCA
 AGTTCTAAAATCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATCTCTCA
 TGCTGCGCAAAGTGCTCGAATAACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
 CATCAACTGAGTATAAAATTTGTATTGATATTCCACCACCTATATCAGAAAAACAGAAAAAA
 TGTGTAAATGTCACCACCAAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC
 CACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
 GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
 AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
 AGAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCCT
 AAAAAACCACCAAGGAAACCTACTCCAAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLLOQTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTPELPEKCLSELSNLQELYINHNLLSTISPGAFIHLNLLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLEISFYDNRL
IKVPHVALQKVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSPNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGGQNVQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEAPQPEIYWITPSGQKLLPNTLTDFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLGIIGVICLISCLSPMNCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

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GCCCGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
 CTGCAGCCTTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
 CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
 GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA
 TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG
 GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
 AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG
 ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
 GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
 TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
 ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC
 AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
 CAACGACGCTGACCCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
 TGTTTGCGTGGTTCACATATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
 GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
 ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA
 GTAGTTTTCGATTGCAGTAGAAATAAGTGTTTACTTCTCCCATCCATTGTAAACATTTGAA
 ACTTTGTATTTTCACTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA
 TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
 AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
 AATTTAAAAGCAAATAAAAGCTTAACTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDSDNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNR
IQSVHKNAFNNLKRARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
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ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATGAGCAGGTGAGCAAGAGGATGCTGGCGGGG
 GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGCTGCT
 GGGCTCAGTGCTGTAGGCTCGGCCACGGGCTGCCCGCCCGCTGCGAGTGCTCCGCCCAGG
 ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGGCATCCCCACCGAG
 ACGCGCCTGCTGGACCTAGGCAAGAACC GCATCAAAACGCTCAACCAGGACGAGTTCGCCAG
 CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGCGC
 CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
 CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT
 CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
 ACAATGACCTCGTCTACATCTCTCACC GCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
 ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCT
 CATCGTCTTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
 TGTACCGACTCAAGGTCTTGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAAC
 TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
 CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCTCAACCTCTCTCAACCCCATCA
 GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
 GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGTCTCAA
 TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
 AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGG
 CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCGAGTTTGTCCA
 GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCACTACTTCACTGCCGCCGCG
 CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT
 GTGTGCCGGGCGGATGGCGACCCGCCGCCCGCCATCCTCTGGCTCTCACC CCGAAAGCACCT
 GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
 ACGCCCAGGTACAGGACAACGGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC
 TCCATGCCCGCCACCTGCATGTGCGCAGCTACTCGCCGACTGGCCCCATCAGCCCAACAA
 GACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
 TGCCTTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
 CTGGGCGTCTCTCTTCTGCTTGGTGTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
 AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
 ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGCGGGGGGCAGGGACCCCCG
 GGCGGCCGGGCAGGGGAAGGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCTTCTCCACCTC
 CTCCCTACCTTCTACACACGTTCTCTTCTCTCCCTCCCGCCTCCGTCCCTGCTGCCCCCG
 CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCAGACCTGGGGACCCCA
 CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA
 ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACTTGGGTTTCAATAATTATGGATTTT
 TATGAAAACCTTGAAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLSLEQLTLEKCNLTISIPTALSHLHGLIVLRLRHLNINAIIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLA VRHLVYLRFLNLSYNPISTIEGSM LHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFH SVGNLETLILDSNPLA
CDCRLLWVFRRRWRLNFNRRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDP PAILWLS PRKHLVSAKSNGR LTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGND SMPAHLHVR SYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTAGGCTCGCCAGCGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC
TGTTTCGCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAACCTTCACTGTGACGAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTG
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTATCTTAGAGGCGCCTGCCCACTTCCTGC
GCCCCCAGGGGCCCTGTGGGGAAGTGTGGGGCCGTCACCAACCCGGACTTGTAACAGAGCAA
CCGCAGGGCCGCCCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGGAGGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCGCTGGCTTCTCTGCATTTGGGTTATTATTATTTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACA
AACAAAAACA

FIGURE 32

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVVKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRILVTSTPHELSSISISNVALADEGEYTCSTFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHLHCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLRHKGTYLTAEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCTTTTCTTCTCCTTTCTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA
TCTGTTCCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGTCTGCAGCGTTTCACTGCCCCGACTTCCAGTTTTACCATTTATTTCTGCATGGCAATTC
CCTCACTCGACTTTTCCCTAATGAGTTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTTCGGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAAATGGCTGGAAAACATTCCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCCTTAGCTAACA
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCCAGGGTCCGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA
GCTTTTCCCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA
GAACGCTTGGGTTCGGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTTCGCACAGTAAAAACAGCACTGGGTGGCGGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
GTTTGTACCTCCGCCTTCAACGTGGTGGGCATGCTCGTGTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG
ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAATAAAGTGTGAGCTCGACAACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTTGAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCAGCACGACCCTGCTGGAAG
AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCCTGTGGGGTTGGATGCCGCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
TGTAATAAGTAACTTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLPNEFANFYNAVSLHMENGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPEYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGK
IPGNWQIKIRPTAAIATGSSRNKPLANSPLCPGGCSCDHIPGSGGLKMNCCNNRVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLLEYLNVEYNAIQILILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNWECSTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFVTSFTVVGMLVFILNRNRKSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTTGACCCAGAAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGC
CGCTGGGCCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCCTCAG
AGAATGAGGCCGGCGTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCCGGCGG
CGGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTCGGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG
GCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGCACTGGAGCGCAGGCGTTCCCACT
GCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTGGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTTGCCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCCTTGGGGGGACCGGGGTGCCACCAGGCGCCCCGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
ACCACTTGTCCCTGAACAAGACAATTCAGTAACATCTATTCTGAGATTCTCGATGGGGAT
CACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCTCTGCCACTCCTCAGGCTTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTTGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCCTCTTCCCAGCCA
AGGAAGGAGTCTATGGGCCCCGCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTTGCTGGCGGAGTCCCCTCTTGGCTCTAGTGATGCATAGGGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGGAACCAAGAGGAACTTAC
TTGTGTAAGTGAACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAA
TTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACA
TTAAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCTAGGCTAGGAGTAT
ATTGGTTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWP I RVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLES DPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGCCGCCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCGCCGTGGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAAATCA
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCATAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTCTTATTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTAGGCCAAAA
AACTGCCTACAACACAGAACAGCCTGTCAACCACCATTTCCCTGTAACCACGGGTTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAAACCATCACTCGCGATGGGAGTTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTACAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCTGTCAAGCAGTGGCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAACAGTGAACGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT
TCTCAGTAGAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCTGCTGTGAGAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT
GTTATTTGTTTACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTA
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLTLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTCCGCTTGT
TTTGGCCCCCTGTGCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTGGAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
TCTGTGTTACACACATCCCCACACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCTTGAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 40

COOPER

AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGTRTPQVVSLPNMRVQKSCASD GALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

[illegible]

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTACAGTGGCCTGATCGCGAATGGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAGCACCCCGTGCCTTCAGCAACTCTTCCTATGTCCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGT CATCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAT
CTTGGTTTTTTGGCATCTGGTTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTGTCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTTCTACCACTGCTGAGTGGCCTGGAACTTGTTTAAA
GTGTTTTATTCCCATTCTTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGGTTCGCAGGAATCTGCACTCAACTGCCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTTCCTTGTTGTTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCCTTCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCTGTTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGCGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYSGFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGT YTCMVSEEGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCAATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCCT
GGAGGCCGCCGCGAGCCCGCTTTCCACCCGACCTCTGCCCAGGCCGAGGCCCCAGCTCAG
GCTCGTGGCCACCCACCAAGTTCAGTGCCGCACCAGTGGCTTATGCGTGGCCCTCACCTGG
CGCTGCGACAGGGACTTGGA CTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCAACGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

[illegible]

Signal sequence:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTGATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGTCT
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCTCCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCACTGGGT
GTTGTTCCCTAAGAAACTGATTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTTCTTCTCTTGGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAAGNAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLLVILARMFQTKFAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTCTGGGGGGCGCACCCGAGTCGGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA
AAGTTCAATTGAAAACCTCTTGCCATCTGATGGTGA CTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGA CTGATGGCAGCATAT
CACAATTTAGGA ACTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA
CCGGTGCAACATGAAGAACAATTTCA TTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCA TTTCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGA AAACCACCTCTGTTTTCTTGCTCTATACAG
CAGCACATATTATCATAACAGACAGAAAATCCAGAATCTTTTCAAAGCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLIKFIENLLPSDGD FWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLL LV
VTTVVCWWICRKRKREQPD PSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAATC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGGAGGCCATCATCAT
CCCACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMOVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCCTTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTTCACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTGCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACCTACATCA
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACTTTATTTACAATAATAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSVPVEGVRLADGPGHCKGRVEVKHQNQWYTVQCOTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCCTGCTGTTTCGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAAACTAGAAATAAACATCTCAAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVDDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRGVMDTTT
AQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA
GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
GGCATTTCCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGAGGCCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT
CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACCTGTTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

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FIGURE 58

MKFLLDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDSCNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

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FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCGCGGCTC
AGGGAGGAGCACCAGCTGCGCCGCACCCTGAGAGATGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA
CCTTGCGTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCATAATTAGTTTTTCCAGATATTTCTGAATATAAAAAATA
ATGACTTTTTATGTCAGTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTTGGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACATATAGTTGAAAAGTACTTGCGAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAAGTTTGAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGAAGTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTATGAAAAGGATGGGATCCTTATGTTGGATATAACTACCTTCCAAAAGAGAACAT
CAGAGGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGC
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGTCTTGAAATAGGAAGTTTTAATTTCTTCTAAGAGTAAGTGAAAAGTGCAAGTTG
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA
TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA
AAAATATTATATATAAAAGTAAAAA

CCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCGCGGCTC

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGD SGQPLFLTPYIEAGKIQKGRELSL
VGPFPG LNMKSYAGFLT VNKTYNSNLF FWF FPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNM TLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F
FQIFPEYKNND FYVTGESYAGKYVPAIAH L I H S L N P V R E V K I N L N G I A I G D G Y S D P E S I I G G
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV TG
CSNYYNFLRCTEPEDQLYYVKFSLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVL IYNGQLDIIVAAALTE RSLMGMDWKGSQ EYKKA EKKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT
TTTTCCCTTTCTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCCCTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCTGGGTC
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGAAGTGGACCTTCAACCACTTGACCGT
CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCTCATCGTGACGCCCTGCAGCGAAGTGCTCACCCCTACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCA
GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT
CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG
CTCTGCAAGGATGACCCCAAGTTCACCTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
ATTACCTCCTCAGCAAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTTCTTGGGGAACAAAGGTGAATGGGGAGGTAAGAAGGGGTTAATTTGTG
ACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCCAAACCTTTAAGAAAAAAGCTTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLAGSL
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESAMLDYELHSDFFVSSLIKIPSDTLALVSHFDIFYIYGFASSGGFVYFL
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPDDSAFCFAFPRAINLQIKERLQSCYQEGEN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCNSAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCGCGCTTAGAGAACACGCGATGACCA
CGTGGAGCCTCCGGCGGAGGCCCGCCGACGCTGGGACTCCTGCTGCTGGTCTGCTTTGGGCTTCCTGGTGCTCC
GCAGGCTGGAGTGGAGCACCCTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTTCGTCTGATGGCCGCAGAGATCG
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACC
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG
GTTCTTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTTGTGGAACCTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGCCACCATCAACTTGCAGT
CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT
ACTGGACGGGGTGGTTTACTCGTGGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTGAACACCGTGT
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG
GAGCCATGCACCTTCCATGACTACAAGTCAGATCACCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGCTGAGGATCTTGGTGGAGAATCGTGCGCGAGTCAACTATGGGGAGAATATGATGACCAGCGCAAAG
GCTTAATTGGAATCTCTATCTGAATGATTCAACCCCTGAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTTTCAAGAGTTTGGCCTGGACAAATGGNGTTCCTCCAGAAACACCCACATTACCTGCTTTCTTTTGG
GTAGCTTGTCCATCAGCTCCACGCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTGTATTCA
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCCAAGACGCTTTACCTCCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTATCGTTTTTGGAGGACGATGGCGGGCCCTGCATTACAGTTACCGGAAACCCCCC
ACCTGGGCAGGAACCAGTACATTAAGTGAAGCGGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTC
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGGCTACAGTCTGCCCCGTGTCTCAGCTCAAAACCTTAAGCCTGCAGGGAAAGGTGGGATGGCTCTGGGCC
TGGCTTTGTTGATGATGGCTTTCTACAGCCCTGCTCTTGTGCCGAGGCTGTGGGCTGTCTCTAGGGTGGGAGC
AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGCACCGGACGTACAGCCC
TGCGAGCATCTGCTGGACTCAGGCGTGTCTTGTGCTGGTTCCTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTCACCAGTGTAGAGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCTTCAACCTTCTGAGCCTTCTTTGGGATTCTTGAAGGAACCTCGGCGTGAGAAACATGTGACTTCCCCTT
TCCCTTCCCACTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG
ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCGAACAGCAGGGGCAGAGCAGCCCTCCTTC
GAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCCTGA
GTTGCAGTAAAGCTATAACCTTGAATCACA

FIGURE 64

MTTWSLRRRPPARTLGLLLLVLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHVFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMSRVVPLQ
YKRGGP IIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKGLSKGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPKMVM EYWTGWFD SWGGPHNILDSSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY TAKYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE
TSITSSGILSGHVHVRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXS L PETPTLP AFFLGSLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGGCTCGGCCCCGAGGCCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCCTGCCTTCGTTCCTTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA
GGCAGACACTCGGTTCGTTCGTAGTGGATAGGGGTTCATGACCGGTTTCTCCTAGACGGGGCCC
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTTCGGGTACCGCGGGTGCTTTGGGGCCGAC
CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTTGAACCTA
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTTCCTTGCCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTTCAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGG
AGAAAAGATCTTGCTCTTCACCAAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACTGTAGATTTTGGCCCAGCTGACAACATGACCAAATCTTTACCCTGCTT
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTTGCTCTTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTTGGGACCTTTACCTCCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCTAGACTTGGCTTTGCCCCCGTGGGGCCAT
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
GAACCTATATGACCCATACCATTTTTGAGCCAACACCATTCCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAG
AGACAAACTATTTTTGACGGGGAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
GGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTTCCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCTCTACGTGCCAAGATTCCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC
CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCTTTTCTAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGGGCGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIF
TL LRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDFTFLYL
PGWTKGQVWINGFNLGRYWTKQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
CTTGTCAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTGCGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAACT
AATTCCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA
CCTTCGAGAGTTGTAATAAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT
GACTTGTTTAAAATTATGGCATAACAAAATTGTTACTATTCCTCCCTCTATTACCCATGTCA
AAAATTGGAGTCACTTTATTTCTTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG
CTTGACCGCCTGCCAGCCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTTG
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCTTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGGTTTTAAGTCATTTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTAAATTGTTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIIICVYGFIPLYTLFWLFRIPPLKEYSFEKVVREESSFSDIPDVKNDFAFLLHMVDQYDQLYSKRFGVFLSEVSENKLRREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSGLVPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESRLRLRHLKILHVKSNIITKVPSNITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCERIPHAIFSLSNLQELDLKSNNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESPLVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDLPLEVKEALNQDINIPFANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCTTTTCATTGACAAACTGACTTTTTTTTATTTCT
TTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT
CTGTGTTTGGGGTTTCTTCTCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCACGTGG
GCTCAGTGCTTGCTTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATATGCCTGTC
ATCGCTGGTGGTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCGTGCTCTGTCTTTACTTCAAAATACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAAACCAGACAAGGTGTGGTGGGCCAAG
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGCTCCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC
AGTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAAA
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGGCAACCCCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAACCTGACGTTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTGGTCTTAAAGGCTGCCAGCGCCTTGCCAAAATGAGAGCTTGTA
AGAAGGCTCATGCCATTGACCCCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAAGCATCAGAATTATCTTTTCTTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGG
CAAGTCTGCAGTAAAAACGACTATGTTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCCTAACATCTCTATTCCAAACTGT
GGCGGTTACCTGGATACCTTGAAGGATCCTTACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTTAACTTCAAAGAGATTTTCTTAGAAATAGAC
AAACAGTGCAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCACCTTCGAATCGTCATCAAACCTCTCTGACTGTCGTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTTTCTGCTTCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA
GACCCAACTTGACAGACCAAATTTATCAAATGTTGTGGAATTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC
CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACCTGGGCAAATATAACACCAGCATGGCTCTTTTGAATCCAATTCA
TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACCTCTTTTGTTCAGTTAGTCTGCAC
ACCTCAGATCCAAATTTGGTGGTGTCTTGTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAACTTGTAAAGGTATCCCTTATTTGGACACTATGGGAGA
TTCCAGTTTAATGCCTTTAAATTTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTGTGATGTGAT
AGCAGTGACCACAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG
AAAACAGATTCCATCATAGGACCCATTCTGCTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTTGAGCAT
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAGTGTGCATCTGTTTCTTTCATGGTTCTAGCTCTG
AATGTGGTGAAGTGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAA

FIGURE 70

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDPDGSCSENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTIKLESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASTYDLIKSGCSRDETCVKYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLI CDSSDHQSRCNQCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVAITITVRHFNQADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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[illegible]

Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

Leucine zipper pattern.

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGC
AGCTGAATTTACAGAAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGAGGA
TGGATTTCGTGGTTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA
AACTGCAACACAAACAACAGAAATTTATTGTCAAGTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCCCTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTGATTTGTGTACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTTTGGTGTGCTGAGCTGGTCTTGGATTTTGC
TATGTCAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCTAATAATATCCCCTGGGAGAAAGGAGTTTTGCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGAC
CCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTA
AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAATAAAAACCTTTATAAATTTCTATTTTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTTCA
GTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTTTATTTTTTGCTGAGACTAATCTT
ATTCATTTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG
TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA
AGCATTTAGAAAACCTT

FIGURE 74

MARCFSLVLLLTISIWTTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

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FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTCCGGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
TCTTTTCTTCCGCTTGGATATTTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATAACCAGCGGGCCAAGAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATT
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAACCTGTTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTTCCCTCCAAGCTTGGGTCACTGTGTTAACTGCTTATC
AGCTATTCAGACATCTCCATGGTTTCTCCATGAACTCTGTGGTTTCATCATTCCCTTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAATTTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCAC
TAACCCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCGGTAATAAAAAGATTGGGATT
TCCTTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG
GGGCCCCAGCCTGGCCCCGGGTACCCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA
TTGCTCCTGCTGCCCCGGCTCCTACGGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCTGTTACCTACCAAGGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAAGCT
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCA
ACGGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG
GTGGCCTCCTTTGAGCAGCTCTTCCGGGCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCCGGCAGCCCTGCGGTGGCC
CAGGCCTGGCACCTGGCGTGCGAAGCTACGGCCCCCGCCACCGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC
AGCTCTTTGCCGCTTGAAGTTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCCAGAGCCTGGGGT
CCGAAGCTTTGGCTTCCCCGACCCGCAGAGCCGCTTGTACGGTGTTTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCCTGCCGCATTCCCTCACTGGCTGTGTATTTATTGAGTGGTT
CGTTTTCCCTTGTGGGTGGAGCCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT
TTAAACATTTTTTTTACTATTTTTTTGTAAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTG
GATGCCCCACTCCAGGAATCATGCTTGCTCCCCTGGGCCATTTGCGGTTTTGTGGGCTTCTG
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTGGTGCCAGAGTGGGC
GGTGGCCTGTCTAGAATGCCGCCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCT
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCCTCCGGAGCTGGGCTTTGGGCCTCTCCTGCC
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCCACTGAGGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAACTCCCCCTCCCCGTTCCCCT
TCCCCTCTCGGTTCCAAAGAATCTGTTTTGTTGTCAATTTGTTTCTCCTGTTTCCCTGTGTGG
GGAGGGGGCCCTCAGGTGTGTGTACTTTGGACAATAAATGGTGCTATGACTGCCTTCCGCCAA
AA
AA

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRR LHRYDVFCFATALKGRVYYLEHPEKLT LTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGGCCCCCTGAGCGACGCTCCCCATGATGACGCCCACGGGAA
CTTCCAGTACGACCATGAGGCTTTCTGAGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTGACCCCCGAGG
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCGGGGACTTCCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCCAGGACCAGCCC
CTGGTGGAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTGTGAGCACC CGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCTCCTGCCCCCTGGGCTCTCAGGGACCCCCTGGGTGCGCTTC
TGTCCCTGTACACCCCCAACCCAGGGAGGGGCTGTCATAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCTTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAA
AAAAAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPWVQTERQQ
FRDFRDLNKDGHLDGSEVGHWWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCAGGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTCCCAG
CCTGTCTGTGTCGTCTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTTCACACCGATCCTG
GGCTTCGCTCGATTTGCCGCCGAGGCGCCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
CGGGTCGTCTGTGTCTCTCTCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCGGGGCTCT
GAGGAGGTGACGCGCGGGGCCTCCCGCACCCCTGGCCTTGCCCGCATTTCTCCCTCTCTCCCAG
GTGTGAGCAGCCTATCAGTCACCAATGTCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGGCCCCGCGGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG
TTTTACCAGAGGCTTGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCCAGGGGGCTGCC
CTCTTGAGGAATTTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACCTATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTTCTTTACAGTAACATAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGG
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC
GCCGATTTAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA
GAAGGACCACATGTGGGCCTTGTTCAAGCCAGTGAACATCCCAAATAGAATTTTACTTGAA
AACTTTACATCAGCCAAAGATGTTTTGTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
ATCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTTCTTACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAATCTCGGACATTGGTGCCAAGAT
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA
AAGAGAATGTCTAGCTGTATCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAA
CTTCTAGTAATTGTACAGATGGGCAGTCTTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCACAAGAGAGTTCACAGGATT
AGAACCAATTGTTTCTGATGTCATCAGAGGCATTTGTAGAGATTTCTTAGAATCCCAGCAAT
AATGGTAACATTTTGAACACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT
CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAACCTATTAAGTATGTCAAC
AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT
ACTTTGTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEF SVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASF T VT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRGNSNTGKAL
KHTAQKFFTVDA GVRKGIPKV VVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVT FVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAF T TREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCCGCACCCGCGGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCC

GGCGGCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCCGGCTCTCAGCTACCCGCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG
TGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT
GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTACA
TCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGC
TCCCCAGGCTGTTCTCAGGCTTCCAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTTTTGGGAAATGTGGAGAAGAGTGGCCTGCTTTGCAAACATCAA
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTG
TGCTTTCAGCTGTTGCAGATGAAATGTTCTGTTTACCCTGCATTACATGTGTTTATTCATCC
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCAATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAACATAATTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC
AGTGTGGGGCAGCCGTCCCTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT
TGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCATAACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA
TAAGCATGCTTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEAAAASSEVNLANLPSPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMMLCTRDSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

[illegible]

AAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMMFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNL
ELTKLDITNNPRLSFIHPRAFHHLPMETLMLNNNALSALHQOTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRRLTPAHAGRRYRVYPEGTLELRRVTAEAGLYT
CVAQNLVGADTKTVSVVVGRALLQGRDEGQGLELRVQETHPHYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCGCTGTTTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGTACCGCACCTACCGCTGTGCCACCC
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCCGTCTTCCTGTGCGGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCCCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC
CAGCATTGCCAGCTCACGGGCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT
GGCCTTCCTGCGGAGAACCTGCGGGCGCTGCACATCAAGTTTCACCGACATCAAGGAGATCCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAACGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCAGCACCT
GCACCGCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCTCCCTGCCGACATCGGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCACTGCCCTCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG
CAACCGGCTGGAGTGCCTGCCTGTGGAGCTGGGCGAGTGGCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGGAG
GCCGGCCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCCGAGGGGCGAGGCCCTAGCTTCTCCAG
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGGCTGGCCCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG
CTGCCACCAGAGGTCTGGGACCCCTCACTTTAGTTCTTGGTATTTATTTTTCTCCATCTCCACCTCCTTCATCC
AGATAACTTATACATTCCCAAGAAAGTTAGCCAGATGGAAGGTGTTTCAAGGAAAGGTGGGCTGCCCTTTCCCC
TTGTCCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCAG
CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCCTCCAGCTGGA
AAGGCCAGGCCTGGAGCTTGCTCTTCAGTTTTGTGGCAGTTTTAGTTTTTGTTTTTTTTTTTTAAATCAAA
AAACAATTTTTTTTTAAAAAAGCTTTGAAATGGATGGTTTGGGTATTAAGGAAAAAAGAAAAAAGCTTAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTTCCCTTGAGCAAAGCAGCCAGACGT
TGAAGTGTGTTTTCTTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTTTCTGGGAGGGAGGTTTTTTTTGTTTTGTTTTTGGGTTTTTTTTGGTGTCTTGTCTTTCTCTCTCC
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGATGAACGGTGTCTCATTCGCACCTCCCCCTCCTCGTGCTGCCCTGCCTCTCCA
CGCAGAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTTCCCCACCTCCTGCGGCATGGGTGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCATCAGCCCTGTGCGCCACCTGGTCTTTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGAGGTGCGCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGC
CTGGAGTGACACAGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCCTTAGATCAATCAGTGGACACTAAGGCAGTTTTAGAGTCTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTGTGTCTTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGTCTGAACTTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAAAAAAAAAAAAA

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FIGURE 88

MRQTIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSIGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSEAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRLHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCTTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCCTTGGGTGATTCTGGATCTCCCCCTGTTGATTGCGGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTAAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCAGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACCATGGGTGAGGAGGCCTG
GGTGCGGAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELWGKAEMIIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMAKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGGCATCGTGCGGTGGAGAGGACGCCGAACCTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTTTGAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAACA
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTTGAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWSGVGCRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT
CTTTGCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCCTGGGCCGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTGGGATCCCAG
CTCTCCTCAATACGGAATAACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGCAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGGTAACCCCTCTGTGATCCGTAAGCGATAACAATTGACCTCACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCCTCAGGTGACAGT
GGGGCCGGGTGTGGTCTGTCTCTGGAAGACACCAGTTCGGCCCTACCTTCCCTGCCTCCAG
CCCCTATGTCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCTCATCACAATGAAA
TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC
CAGTGGCCGTGCCATACCAGATGTGGCTGCACTTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGTTTGGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCCAGCTTTGCTGGAAGACTCTACTCAACCCCTGACCCTTTCCTATC
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCAGTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTGACTCCCAACCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCTTAGATTCCCTCAATAAGATGCTGTAACCTAGCATTTTTTTGAATGCCTCTCCCTCCGC
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCAATCCCCAATTCAGTGCAAGGAGACCTCTACTGTCACCGTTTACTCT
TTCTTACCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATG
GCCTTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACTTCTCTG
ACTACTCTTGTCTTCCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC
TCCATTTGTAGATTTTTGCTCTTCTCAGTTTACTCATTGTCCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA
TGTAACAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

[illegible][illegible]

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKL RVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCCTGTTTCAAGGACAACCTGAACAAACCATAACCTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCCTGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCCTGCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCTGCAGAAGCTGAAGGTTCCATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGGCCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCCGAC
GGCCTCAGGCCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCAC
GACTTCCGGCCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATT
CTCCAAAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318

><subunit 1 of 1, 317 aa, 1 stop

><MW: 33732, pI: 7.90, NX(S/T): 1

MVVGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPIITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACCTGAGGCCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACCTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCCCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCCCTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG
TGAAGAGGTCAGCTGTCTCCTGTCTCTTCCCCACCCTGTCCCCAGCCCCTAAACAAGATA
CTTCTTGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAAGCTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSP TASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVWAKTERIGCGSHFCEKLGQVEETNIELLCVNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSF RATEASDSRKMGT PSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSV
SGLNSGPGHVWGPLLGLLLLLPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAAGTGAAGTCAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAATTTCGGTCATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTGTTCTCCCTCTGCTTGCCTTTTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTTCAT
CAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAATGAATTGGAGACCATTTC
AAATCTGGGACCAGTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTAGAGCTCCAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAA
TTTGGCCAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAGATGTTTAAACT
GCCCCAAGTGAACATCTCGAATTGAACCGAAAACAAGATTAAGAAATGTAGATGGACTGACATTCCAAGGCCTTGG
TGCTCTGAAGTCTCTGAAATGCAAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAA
CATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCT
GCAGGAACCTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAG
TGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAAATAC
ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCTTCCGGGGGCTTTCCAGTTTAAAGACTTT
GGATCTGAAGAACAAATGAAATTTCTTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAG
GCGACTGATACCTCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAACTGCAACAATT
GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAAACAACCTT
TCAGAGCTTTGTAAATGCCAGTTGTGCCCATCTCAGCTGCTAAAAGGAAGAAGCATTTTGTGCTGTAGCCGAGA
TGGCTTTGTGTGTGATGATTTTCCCAAACCCAGATCACGGTTTCCAGCCAGAAACACAGTCGGCAATAAAAGGTTT
CAATTTGAGTTTTCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTTGTGCTTGGAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAATTTATGCACACCTCCGGGGCCCAAGGTGGCGAGGTGATGGAGTATACCAC
CATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCATCTCCAATCACTTTGGTTT
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCATGGATCTCACCAT
CCGAGCTGGGGCCATGGCAGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGGCACAGACTTTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCGAGGATGACGTGTTCTTTATCGT
GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTAGCAAATGC
AATCTGACTGTCTAGAAACACCATCATTTTTCGGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGC
CGTCTACAGTGCTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCCATTTGGTGGT
AACCAGAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGCTGAGTGGGAA
ATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTGCTGATCATAGC
CGTGGTTTGTGTGTGGTGGGCACGTCACTCGTGTGGTGGTTCATCATATACCACACAAGGCGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCCTAGTTATTTGTCTCATCTCAGGGAACGTT
AGCTGACAGGCAGGATGGGTACGTGTCTTTCAGAAAGTGGAAAGCCACCACAGTTTGTCTCATCTTCAAGTGTCTGG
ATTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC
CACAGATCTGTTCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA
TCCTTTTGAACATATCATAAGGTTGCAGTCTTACCCCAAGAACAGTTTTAATGGACCCTATGAGCCAGTTA
CATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCTTTCAGAAAGTCTTGGCAACCGGAGCTTCAGTAATATATC
GTGGCCTTTCATGTGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTG
TCTAAACAAGTCTCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTTCTTCATGGG
TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTGAGCC
AAGAGCCTTTTATTTGAAAGCTCATTCTTCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAAGAAAGGAC
AGATTTTCAGGAAGAAATCACATTTGTACCTTTAAACAGACTTTAGAAAATACAGGACTCCAAATTTTCAGTC
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTA
AAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGAT
GAACCAAAATTACAAAAAGTTATGAAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTAACTA
TTTTTTAACTTTGTTTTATGCAAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTATGTATTT
TTATAATGCCAGATTTCTTTTATGGAAGTATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTT
TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAATGTGTCAATTTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPV
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRISAIPPKMFKLPLQHLNLRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRILQGNRIRSITKKAFTGLDALEHLDSLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNEELLHDAEMENYAHRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVDSVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVG VVIIAVVCCVVGTSLVWVVI IYHTRRNEDCSITNTDETNPADIPSYLSSQGTLD
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

[illegible]

GGGGAGAGGAATTGACCATGTA AAAAGGAGACTTTTTTTTTTGGTGGTGGTGCTGTTGGGTGCCTTGCAAAAATG
AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAG
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAAGAGTTAGACCCGCGGGGTGGTGTGTTCTGCATAAAATAAATAATCTTAAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCACAAAGAAAAAAGTATGTTTCATTTTTCTC
TATAAAGGAGAAAGTGACCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAAGCT
GGTGTGGTGGTGTCTTTCTTTTGAATTTCCCAAGAGGAGGAGGAATTTAATAATACATCGCAAAAGAA
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTTTAAAT
TTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTGTTCTTAACCACCTGGATTTCCATCTGGATGTTGCT
GTGACAGTCTGAAATAACAACGTGTTGAATTCAGAAGGACCAACACCGATAAAATATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAACAGGGCCCTATTGACCCCTGCTTGTGGTGCT
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCCCTCTGTGTCTCTCGCAAC
CCAGTTTCAGCAAGGTGATTTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT
GCTGAACCTCCATGAGAACAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACCTTGAGGCATTGGAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAATCGTCTTACTACCATCCCGAATTGAGAGCTTTTGCTATCTGTCTTAACTGAAGGAGCTCTGGTT
GCGAAACAACCCCATTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCTTCTTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGC
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATCTTTCTGGGAATCA
TTTATCTGCCATCAGGCCCTGGCTCTTTCCAGGTTTGATGACACCTTCAAAAACCTGTGGATGATACAGTCCAGAT
TCAAGTGATTGAACCGGAATGCCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACAACAATACTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCAACACCTTGAACATG
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCCGTG
TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTCGGGCCTCCACATC
CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACATACAGGAGTACATGATGATGGTGAGTAA
TTCCGTTGGGAATACTACTGCTTCAGCCACCTGAAATGTTACTGCAGCAACCACTACTCCTTTCTTACTTTTTC
AACCGTCAAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCC
AGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACACACAGGCACAAGGTGACAGAGAAAACCTT
CACCATCCCGATGACTGATATAAACAGTGGGATCCCGAATTTGATGAGGTGATGAAGACTACCAAAATCATCAT
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGTCATTTCTACAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTTATTAATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAGGCCACCTGCCCATGCCGTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
CAACCAACAACAACAGTTAAACACAATAAATCTAAATACACAGTTTCAAGTGCATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAACTTGAACCAATTTACAGAGTTACAAAAAACAAACAATCAAAAAA
GACAGTTTATTAATAAATGACACAAATGACTGGCTTAATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACA
AAAAGAAAAGAAATTTATTTATTAATAAATTTCTATTGTGATCTAAAGCAGACAAAAA

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Signal sequence:

Transmembrane domain:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA
TGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACGCGACCGC
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCCCGCTGGGAGCTTCGGGTAGA
GACCTAGGCGCTGGACCGGATGAGCGCGCGCGAGCCTCCGTGCGCGCGCGCGGGTTGGGGCTGCTGCTGTGC
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGCGGTGCGGGGAACCTCGGCGAGCCCTCTGGGGTAGCCGCC
GAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT
CCCAGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCC
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
GTCTCGGCAAATATTACACTTCTCTCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATTTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACA
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCAAGATGTTTAAACTGCCCAACTGCAA
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCCTTGGTGTCTGAAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTTGGGGGCTGAGCAACATGGAAATTTTG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGTGTATGCTGCAGGAACCTCAT
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTCAGCTGCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAAATACACTGCACATTGGG
AACACAGAGTCAGCTACATTGCTGATTGTGCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGTCTTCTCTGGGCTTGACAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTACAAATGAAGAACTGCAACAATTGCATTTAAATACA
TCAAGCTTTTTGTGCGATTGCCAGTGAAGGGAATATGCTCCCAAGTGGGTGGCGGAAACAACCTTTCAGAGCTTTGTA
AATGCCAGTTGTGCCCATCCTCAGCTGTAAAAGGAAGAAGCATTTTTGTGTGTAGCCCGATGGCTTTGTGTGT
GATGATTTTCCCAAACCCAGATCAGGTTTCCGCGAACAACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTATTCCTCAATGACTTTTGTCTGGAAAAAGACATGAACCTACTGCATGAT
GCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTG
CGCGAGGTGGAATTTGCCAGTGAAGGGAATATCAGTGTGTCTCCTCAATCACTTTGGTTTCATCCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCC
ATGGCAGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC
TCCCAGCTGCACGGGAGAGACGCATGCTGATGCCCCGAGGATGACGTGTTCTTTATCGTGATGTGAAGATA
GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTC
CTAGAAAACCATCATTTTTTCCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCTTACAGTGC
ATTGCTGGAGGAAGCCCTCCCTTAACTGAACCTGGACCAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC
TTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGAGTGTGCTGGGAAATACACATGTGAG
ATGTCTAACACCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCACTCCAACCTGCGACTCCCCT
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGTCTGT
GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC
AACACAGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTGTCTCATCTCAGGGAACGTTAGCTGACAGGCAG
GATGGGTACGTGTCTTCAAGAAAGTGAAGCCACCACAGTTTGTCTCATCTTCAAGTGTGGATTTTTCTTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGAAGCTGCCACAGATCTGTTTC
CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAATGTGTATGGCTCAGATCCTTTTGAAACA
TATCATACAGGTTGCAGTCTGACCCAAGAACAGTTTAAATGGACCCTATGAGCCCAGTTACATAAAGAAAAAG
GAGTGCTACCCATGTTCTCATCTTCAAGAAATCCTGCGAACGGAGCTTCAAGTAATATATCGTGGCCTTCACAT
GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
TCTTTAGATTTTGTGCAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTTCATGGGTACCTTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTGAGCAAGAGCCTTTTAT
TTGAAAGCTCATTCTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA
GAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAAAGCTTAACTACTACCTCAAGTGAACCTTTATTTAAAGAGAGAGAAT
CTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTTATACAGATGAACCAAAATAC
AAAAAGTTATGAAAATTTTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTG
TTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA
TTTCTTTTTATGGAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAAATAGAAGTT
ACTTCATTATATTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAA

CCAGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRISAIPPKMFKLPLQHLLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNHLTEITKGWLYGLLMLQELHLSQNAINRISPDWEFC
QKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWLPOWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHAPAQIAWQKGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHF
FAAGNQLLIIVDSVDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDQWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTADRQ
DGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDIFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEEHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

[illegible]

CAAAACTTTCGCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCCTGGGTGGTCCCGTCCCCCTATCCCTCCTTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGGCCGGCTGATCTGCAG
GCGCACGACATTCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCCTGGT
TCCATCAGCCCTGGCGCCGAGCGCATCTGACTCGGCACCCCCTGCAGGCACCATGGCCCCAGAGCCGGGTGCTGC
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGGCGTGAGGCCCCAGGATTTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGTGGTACTGAGCCCTGAGG
AGCCCCGGGCTGGCCAGCCGCGGTGAGCTGCCCCGAGACTGTGCCCTGTTCCAGGAGGGCGTCTGTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCCCGGGGGACCTGCCCTGAGCACACCAACCACCTATCTCTGCAGAACAACCAGC
TGGAAAAGATCTACCCTGAGGAGCTCTCCCGGTGCACCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA
CTTCCCGAGGGCTCCAGAGAAAGGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTTGGCCAATAACAAGC
TGACCTTGGCACCCCGCTTCTCTGCCAAACGCGCTGATCAGTGTGAGACTTTGTCTGCCAACTATCTCACCAAGATCT
ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGCAGACGACCGGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCTCATCTGTCCAGCAAACCTTCTTGCGCCACGTGC
CCAAGCACTGCCGCCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT
TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACCTACCTGACTGACGAGGGCCTGGACAACGAGA
CTTCTTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCCAGCAACACCTGTCTCGGGTCCCAGCTGGGCTGC
CGCGCAGCCTGGTGTCTGCTGCACCTTGGAGAAGAACGCCATCCGGAGCGTGAGCGGAATGTGCTGACCCCATCC
GCAGCCTGGAGTACCTGTCTGTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTTGGCCTTCCAGGGCC
TCAAGCGGTTGCACACGCTGCACCTGTACAACAACGCGCTGGAGCGCTGCCAGTGGCTGCCCTCGCCGCGTGC
GCACCTCATGATCTTGCACAACCAGATCACAGGCAATTGGCCGCGAAGACTTTGCCACCACCTACTTCTTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACAGCCACAGTGCACCGCGACGCTTCCGCAAGCTGCGCCTGTCTGC
GCTCGCTGGACCTGTCTGGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCCTCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGCTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAACA
AGATTAGTGCGGTGCCCCGCCAATGCCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAACAAGC
TGGCTTGTGGGCTCCGTTGTTGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGAACATTGAAGGCAACT
TAGAGTTTGGTGACATTTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAGGAGGAGGAAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAAGTGATGCAGATGTGACTAGGATGATGAGACCGCGGACTCTTTCTGC
AGCACACGCCCTGTGTGCTGTGAGCCCCCCTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACGGCGTGTCCACGGCCAGACACATGC
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACCTACCTCCAAACCACCACAGTCTCTGTACAC
CCCCATACCCGTGCCACGCCCTCTGAATCATGTCAGGGAAGGGTCTGCCCCCTGCCCTGGCACACACAGGCACCCA
TCTCCTCCCCCTGTGACATGTGATGCGTATGCATACACACCAACACACACATGCACAAGTCAATGTGCGAA
CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT
GTCCATCTGTCCGTCCGTTCCTTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCCT
GGAACCTCAAAAAGCTGGCTTTTATTCTTTCCCATCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACTTTTCCAATGGGCAAGCCAGTGAGGAGCAGGATGGGAGAGGCCCCCTGGGTGCTGTGGGGCCTTTGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GTTCTTTCAGGCCTGTGGGGGAAGTTCCGGGTGCCCTTATTTTTTATTCTTTTCTAAGGAAAAAATGATAAAAAT
CTCAAAGCTGATTTTTTCTGTTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPREENEFAEEEPVLVLSPPEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRHRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKHLKNNKLEKIIPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

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FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCCGGGAGCGGCAG
CAGTAGCCCCGGGCGGCGAGGGCTGGGGGTTCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGCGCCCAACCC
CAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCCAACATGGATTTTCTCCTGGCGCTGGT
GCTGGTATCCTCGCTCTACCTGCAGGCGGCCGCCGAGTTTCGACGGGAGGTGGCCCAAGCAAAATAGTGTATCGAT
TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTAGCC
TGTGTGCCAACCACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACCTGTCAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGTATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTACATAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAA
CGTACGTGGGTCCTACAAGTGCAAATGTAAAGAAGGATAACCAGGGTGATGGACTGACTTGTGTGTATATCCCAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTCGATGTGTGAAGTACTTGGTGGCCTCCGAAGACACCATATATCCTCCTATCATTACCAA
CAGGCCCTACTTCTAAGCCAAACAAGACCTACACCAAAGCCAAACACCAATTCTACTCCACCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACCCGGACTGACAACCTATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGATTACAGTTGACAACAGGGTACAGACAGACCCTCAGAAACCCAGAGG
AGATGTGTTTCAGTGTCTGGTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTCCGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCATTGAGGGACCTGTGCCTGTCTATTGAGGCA
CAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGGCAGGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAGGGTTGGAAAAAAGATCTATGATGGAAAATTAAAGGAACTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAACCATTTGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTG
TTCTCCATATGACTAAGAATAGAACAAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAGG
GGCCATTGTTAGAACTTCTATAAAAAAAGAGTGTGAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGA
TAAAAATTTGTTCTATTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTTCCCAA
AGATGTTTTGATCCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
CATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCACCAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTTCAATGTTTCTCATGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAAGAGATCCTTCAAGGAACACAGTTTCAAGAG
ATTTTCATCGGGTGCAATCTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGCCCTGCCCC
ACACCGGCAGACCTTTCTTTCACCTCATCAGTATGATTGAGTTTCTCTTATCAATTGGACTCTCCCAGGTTCCAC
AGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGTCTTCTGTCTATTAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAAATATATGGCTGTAGATCCATTTTTAATGGTTTATT
TCCTTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAAAATAAATGAAAAATTTTACTTTTCGATGCCAA
TGATACATTGCATAAAGTATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTATTATTATTAATGTTTT
CTAAATAAAAAATGTTAGTGGTTTTCCAAATGGCTAATAAAAAACAATTATTGTAAATAAAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGC DVVKGQIRCQCPS PGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDEC SLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKNGTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTLRTPLPPTT PERPTTGLTTIAPAASTPPGGITVDN
RVQTD PQKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLP LGRMLHSGDLCL SFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCTTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACCTTTCTTTCTTTTGCAACAGGTGCTTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTGAGGCCCTCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC
AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTTCATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTGTCACTTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
GTATGAAGTTATTCAGCACATCCCTGCCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG
GCTAAACAGTACATTCGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA
TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTTACATTGTTTCGATTTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG
TTAAGAAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAACTATGCCTTCTCTTTTTTTTCAATCACC
AGTAGTATTTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA
TTTTTTTTCAAGGAAAGATGGATTCAAATAAATTATCTGTTTTTGCTTTTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVGRQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTSLASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNRGPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV
YEVIOHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGACAGTTCCCCTGGCAGTCCTGGTGCTGTT
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTCCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGATTGCCAGTGTGGGGATCATATACT
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGCG
AGATTGCCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATAACCCATAACCTTCAAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGAGGAGGAACAAGAGCGGGATGAAGAA
GATGTTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCATTGTGTTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTGAGAACATAAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTATGTATATTTGT
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAATTTACATTTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG
AAATGTGTATTTGAGTGACAATTTCTGTTGCTTTTTTAGAGGTATATTCCAAAATTTCTTGT
ATTTTLAGGTTATGCAACTAATAAAAACCTTACATTAATTAATTACAGTTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTC
CAACAAAGTTTGATTTTCTCTTGATTTTTTCTTACTTACTATGGGTACATTTTTTTATTTTT
CAAATTGGATGATAATTTCTTGGAACATTTTTTTATGTTTTAGTAAACAGTATTTTTTTGTT
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAATTT
TTGGCCACTTTTTTTCAGATTTTACATCATTCTTGCTGAACCTTCAACTTGAAATTGTTTTTTT
TTTCTTTTTTGATGTGAAGGTGAACATTCTGATTTTTTGTCTGATGTGAAAAAGCCTTGGTA
TTTTACATTTTGAAAATTCAAAGAAGCTTAATATAAAAGTTTGCATTCTACTCAGGAAAAAG
CATCTTCTTGTATATGTCTTAAATGTATTTTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTACAGTCTGTAATGCTTGATGTTTTTAAATAATAACATTTTTTATATTTTTTAAAGACAA
ACTTCATATTATCCTGTGTTCTTTCTGACTGGTAATATTGTGTGGGATTTACAGGTAATAA
GTCAGTAGGATGGAACATTTTAGTGATTTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
CACCTTAAAGAAGGGGGGAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTTCTGTAATGTCCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT
AAAGAGTTTGGATGTGTAACCTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQPSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

[illegible]

CGCAGTGTCCAGCTGCGGAGACCCGTGATAATTCTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
AAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCCTCACCTCTATTG
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTTCGAAGATTAAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGTCAGGACTCAGCTGCA
GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
GAGGGGAACCTTCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTACCCGCCGCTGCTC
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAAACGTTAAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGG
GAGGGTGTCAAAC TGACACCCCGTAGACAGAAAGAGGCTTTTTCTGTAGGTACCACCATGGCAA
CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA
TCGT CAGGTACTACGATGT CATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGACAGAGCCACCGTTTCGTGATCCCAAGACAGGAGTCCTCACTGTCGCCAGCTA
CCGGGTTTTCAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG
CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG
GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAAGACATGCTGCCTGCC
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTGA CATCCTTTTTCTGTCTTCCCTTCCCTTCCCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTCTTATCAGGCT
GATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCAGCCCTTCCATTTCAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTTAT
GGCATTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP
TDEDEIGAALKMRLQDQTYRLDPGTISRGLPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRLLSLDPSHERAGGNLR
YFEQLLEEREKTLTNQTEAELATPEGIYERPVDYLPERDVYESLCRGEQVLTTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEQDYR
TRHAACPVLVGCKWVS NKWFHERGQEFLRPCGSTVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

[illegible]

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FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPD SRARLD
QSDedFKPRIVPYRDPNKPYKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLOGASRADVGDALETALEQLNRRYQPRLRFOKQRLNNGYR
RFDPAARGMEYTLDLLLECVTQRGHRRALARRVSLRLPLSRVEILPMPYVTEATRVQLVLP LL
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAELERRY PG
TRLAWLAVRAEAPSQVRLMDVVSCKHPVDTLFFLTWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEAGCFYNADYLAA
RARLAGELAGQEEEEALEGLEVMDFLRFSGHLHFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQEQA NST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTGAGTATACTGTATTATCCTTGTAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTG
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACC
CAACCAGGTAGTAGAAGGCTGTTGTTTCAAGATATGGCTGTTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGTTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTTCTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTAAACACATGAACATTGTAAATG
TGTTGGAAAGAAGTGTTTAAGAATAATAATTTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTGATTGGTT
AAAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAAATGTACAATAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMWIKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAGAAACAAAAAACCAAAGAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTTCAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAAGCTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCTTACAAGA
AACCTAAAATGAGAGAGTTTTTTTATTGGACTGTCAGACCAGGTTGTCTGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA
ATGATGTAAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTG
AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATACAAATAAAAAATAAGTAGTTTTAAATGTTAAAAAAAAAAAAA
AAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCA TMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCACTGGTACAGGAATTTGAAAGTGTGGAACGTCTTGCATCATTACGGATTTCG
AGACAAGTGACCCCAAGATCGAGTGGAAGAAAATTCAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCTGTCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCTTTGCTCGAAATGACCCGAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACCGATT
CCAGAGCCAATCCCAGATTTTCGCAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTTCAGTGCTG
TTCACAAGGACGACTCTGGGCGAGTACTACTGCATTGGCTTCCAATGACGCAGGCTCAGCCAGGTGTAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTCTTGTGCTGACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTTGCTCAGTAAACGCCCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCAACCACTGGTCTGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT
TACATCTAAATTTTTGCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTTTTTAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT
TGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTCT
CACACAAGTTTTAGCCTTTTTTACAAGGGAACCTACTGTCTACACATCAGACCATAGTTGCTTAGGAAAACCTT
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAATTATTTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT
CCCACTGTTCTCTTTTGGCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAAGCTCAGGTGGAGCAGCCAGGTGAAAGGCCCTGGCGGGGAGGAAAG
TGAAACGCCTGAATCAAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTTCATCCGCCGAGACACTGCTCCCATT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCCTGGA
GAATGGCTCTCACTACTCACCTTGTCTTTGAGCTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTGCCGCGAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT
TCTTGGTTGTATAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCTTAAACCTTCTACACTAGTGCCA
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCATAAAGTGAAGTAGA
CGAAAAGGAATACTCGTGATTTTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTTCT
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTTGTTTAAAC
CTCATTTATAAAAGCTTCAAAAAAACCCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVPCRVKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267